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#2



OIPE

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/016,236

DATE: 03/27/2002

TIME: 10:39:22

Input Set : N:\Crf3\RULE60\10016236.raw

Output Set: N:\CRF3\03272002\J016236.raw

SEQUENCE LISTING

3 (1) GENERAL INFORMATION:

5 (i) APPLICANT: Ryals, John  
6 Friedrich, Leslie  
7 Uknes, Scott  
8 Molina, Antonio  
9 Ruess, Wilhelm  
10 Knauf-Beiter, Gertrude  
11 Kung, Ruth  
12 Kessmann, Helmut  
13 Oostendorp, Michael

ENTERED

16 (ii) TITLE OF INVENTION: METHOD FOR PROTECTING PLANTS

18 (iii) NUMBER OF SEQUENCES: 32

20 (iv) CORRESPONDENCE ADDRESS:

21 (A) ADDRESSEE: Novartis Corporation  
22 (B) STREET: 3054 Cornwallis Road  
23 (C) CITY: Research Triangle Park  
24 (D) STATE: North Carolina  
25 (E) COUNTRY: USA  
26 (F) ZIP: 27709

28 (v) COMPUTER READABLE FORM:

29 (A) MEDIUM TYPE: Floppy disk  
30 (B) COMPUTER: IBM PC compatible  
31 (C) OPERATING SYSTEM: PC-DOS/MS-DOS  
32 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30

34 (vi) CURRENT APPLICATION DATA:

C--> 35 (A) APPLICATION NUMBER: US/10/016,236  
C--> 36 (B) FILING DATE: 12-Dec-2001  
37 (C) CLASSIFICATION:

77 (vii) PRIOR APPLICATION DATA:

40 (A) APPLICATION NUMBER: 08/996,685  
41 (B) FILING DATE:  
45 (A) APPLICATION NUMBER: US 08/761,543  
46 (B) FILING DATE: 6-DEC-1996  
49 (A) APPLICATION NUMBER: US 60/034,378  
50 (B) FILING DATE: 27-DEC-1996  
53 (A) APPLICATION NUMBER: US 60/034,379  
54 (B) FILING DATE: 27-DEC-1996  
57 (A) APPLICATION NUMBER: US 60/034,382  
58 (B) FILING DATE: 27-DEC-1996  
61 (A) APPLICATION NUMBER: US 60/034,730  
62 (B) FILING DATE: 10-JAN-1997  
65 (A) APPLICATION NUMBER: US 60/035,021

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66      (B) FILING DATE: 10-JAN-1997
69      (A) APPLICATION NUMBER: US 60/035,022
70      (B) FILING DATE: 10-JAN-1997
73      (A) APPLICATION NUMBER: US 60/035,024
74      (B) FILING DATE: 10-JAN-1997
78      (A) APPLICATION NUMBER: US 08/875,015
79      (B) FILING DATE: 16-JUL-1997
82      (viii) ATTORNEY/AGENT INFORMATION:
83          (A) NAME: Meigs, J. Timothy
84          (B) REGISTRATION NUMBER: 38,241
85          (C) REFERENCE/DOCKET NUMBER: PF/5-21215/P1/CGC1912
87      (ix) TELECOMMUNICATION INFORMATION:
88          (A) TELEPHONE: (919) 541-8587
89          (B) TELEFAX: (919) 541-8689
92      (2) INFORMATION FOR SEQ ID NO: 1:
94          (i) SEQUENCE CHARACTERISTICS:
95              (A) LENGTH: 5655 base pairs
96              (B) TYPE: nucleic acid
97              (C) STRANDEDNESS: single
98              (D) TOPOLOGY: linear
100         (ii) MOLECULE TYPE: DNA (genomic)
102         (iii) HYPOTHETICAL: NO
104         (iv) ANTI-SENSE: NO
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108             (A) NAME/KEY: exon
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110             (D) OTHER INFORMATION: /product= "1st exon of NIM1"
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119             (B) LOCATION: 4271..4474
120             (D) OTHER INFORMATION: /product= "3rd exon of NIM1"
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123             (A) NAME/KEY: exon
124             (B) LOCATION: 4586..4866
125             (D) OTHER INFORMATION: /product= "4th exon of NIM1"
127         (ix) FEATURE:
128             (A) NAME/KEY: CDS
129             (B) LOCATION: join(2787..3347, 3427..4162, 4271..4474, 4586..4866)
132         (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
134 TGTGATGCAA GTCATGGGAT ATTGCTTTGT GTTAAGTATA CAAAACCATC ACGTGGATAC      60
136 ATAGTCTTCA AACCAACCAC TAAACAGTAT CAGGTCATAC CAAAGCCAGA AGTGAAGGGT      120
138 TGGGATATGT CATTGGGTTT AGCGGTAATC GGATTGAACC CTTTCCGGTA TAAAATACAA      180
140 AGGCTTTCGC AGTCTCGGCG TATGTGTATG TCTCGGGGTA TCTACCATTT GAATCACAGA      240
142 ACTTTTATGT GCGAAGTTTT CGATTCTGAT TCGTTTACCT GGAAGAGATT AGAAAATTTG      300
144 CGTCTACCAA AAACAGACAG ATTAATTTTT TCCAACCCGA TACAAGTTTC GGGGTTCTTG      360

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146 CATTGGATAT CACGGAACAA CAATGTGATC CGGTTTTGTC TCAAAACCGA AACTTGGTCC 420
148 TTCTTCCATA CTCCGAACTC TGATGTTTTT TCAGGATTAG TCAGATACGA AGGGAAGCTA 480
150 GGTGCTATTC GTCAGTGGAC AAACAAAGAT CAAGAAGATG TTCACGAGTT ATGGGTTTTA 540
152 AAGAGCAGTT TTGAAAAGTC GTGGGTTAAA GTGAAAGATA TTAAGAGCAT TGGAGTAGAT 600
154 TTGATTACGT GGACTCCAAG CAACGACGTT GTATTGTTTC GTAGTAGTGA TCGTGGTTGC 660
156 CTCTACAACA TAAACGCAGA GAAGTTGAAT TTAGTTTATG CAAAAAAGA GGGATCTGAT 720
158 TGTTCTTTTCG TTTGTTTTCC GTTTTGTCT GATTACGAGA GGGTTGATCT GAACGGAAGA 780
160 AGCAACGGGC CGACACTTTA AAAAAAAT AAAAAAATG GGCCGACAAA TGCAACGTA 840
162 GTTGACAAGG ATCTCAAGTC TCAAGTCTCA ATTGGCTCGC TCATTGTGGG GCATAAATAT 900
164 ATCTAGTGAT GTTTAATTGT TTTTATAAG GTAAAAAGGA ATATTGAATT TTGTTTCTTA 960
166 GGTTTATGTA ATAATACCAA ACATTGTTTT ATGAATATTT AATCTGATTT TTTGGCTAGT 1020
168 TATTTTATTA TATCAAGGGT TCCTGTTTAT AGTTGAAAAC AGTTACTGTA TAGAAAATAG 1080
170 TGTCCCAATT TTCTCTCTTA AATAATATAT TAGTTAATAA AAGATATTTT AATATATTAG 1140
172 ATATACATAA TATCTAAAGC AACACATATT TAGACACAAC ACGTAATATC TTACTATTGT 1200
174 TTACATATAT TTATAGCTTA CCAATATAAC CCGTATCTAT GTTTTATAAG CTTTATACA 1260
176 ATATATGTAC GGTATGCTGT CCACGTATAT ATATTCTCCA AAAAAACGC ATGGTACACA 1320
178 AAATTTATTA AATATTTGGC AATTGGGTGT TTATCTAAG TTTATCACAA TATTTATCAA 1380
180 CTATAATAGA TGGTAGAAGA TAAAAAAT ATATCAGATT GATTCAATTA AATTTTATAA 1440
182 TATATCATTT TAAAAAATTA ATTAAAAAGAA AACTATTTCA TAAAAATGTT CAAAAGATAA 1500
184 TTAGTAAAAAT TAATTAAATA TGTGATGCTA TTGAGTTATA GAGAGTTATT GTAAATTTAC 1560
186 TTAATAATCAT ACAAACTTTA TCCTAATTTA ACTTATCATT TAAGAAATAC AAAAGTAAAA 1620
188 AACGCGGAAA GCAATAATTT ATTTACCTTA TTATAACTCC TATATAAAGT ACTCTGTTTA 1680
190 TTCAACATAA TCTTACGTTG TTGTATTCAT AGGCATCTTT AACCTATCTT TTCATTTTCT 1740
192 GATCTCGATC GTTTTCGATC CAACAAAATG AGTCTACCGG TGAGGAACCA AGAGGTGATT 1800
194 ATGCAAGTTC CTCTCTCTTC TCAGTTTCCA GCAACATCGA GTCCGGAATA CACCAATCAA 1860
196 GTGAAGGATG AGCCAAATTT GTTAGACGT GTTATGAATT TGCTTTTACG TCGTAGTTAT 1920
198 TGAAAAAGCT GATTTATCGC ATGATTACGA ACGAGAAGTT GAAGGCAAAT AACTAAAGAA 1980
200 GTCTTTTATA TGTATACAAT AATTGTTTTT AAATCAAATC CTAATTAAAA AAATATATTC 2040
202 ATTATGACTT TCATGTTTTT AATGTAATTT ATTCCTATAT CTATAATGAT TTTGTTGTGA 2100
204 AGAGCGTTTT CATTTGCTAT AGAACAAGGA GAATAGTTCC AGGAAATATT CGACTTGATT 2160
206 TAATTATAGT GTAAACATGC TGAACACTGA AAATTACTTT TTCAATAAAC GAAAAATATA 2220
208 ATATACATTA CAAAACTTAT GTGAATAAAG CATGAACTT AATATACGTT CCCTTTATCA 2280
210 TTTTACTTCA AAGAAAATAA ACAGAAATGT AACTTTCACA TGTAATCTA ATTCTTAAAT 2340
212 TTAATAAATA ATATTTATAT ATTTATATGA AAATAACGAA CCGGATGAAA AATAAATTTT 2400
214 ATATATTTAT ATCATCTCCA AATCTAGTTT GGTTACAGGG CTTACCGAAC CGGATTGAAC 2460
216 TTCTCATATA CAAAAATTAG CAACACAAAA TGTCTCCGGT ATAAATACTA ACATTTATAA 2520
218 CCCGAACCGG TTTAGCTTCC TGTTATATCT TTTTAAAAAA GATCTCTGAC AAAGATTCCT 2580
220 TTCCTGGAAT TTTACCGGTT TTGGTGAAAT GTAAACCGTG GGACGAGGAT GCTTCTTCAT 2640
222 ATCTCACCAC CACTCTCGTT GACTTGACTT GGCTCTGCTC GTCAATGGTT ATCTTCGATC 2700
224 TTTAACCAAA TCCAGTTGAT AAGGTCTCTT CGTTGATTAG CAGAGATCTC TTTAATTTGT 2760
226 GAATTTCAAT TCATCGGAAC CTGTTG ATG GAC ACC ACC ATT GAT GGA TTC GCC 2813
227 Met Asp Thr Thr Ile Asp Gly Phe Ala
228 1 5
230 GAT TCT TAT GAA ATC AGC AGC ACT AGT TTC GTC GCT ACC GAT AAC ACC 2861
231 Asp Ser Tyr Glu Ile Ser Ser Thr Ser Phe Val Ala Thr Asp Asn Thr
232 10 15 20 25
234 GAC TCC TCT ATT GTT TAT CTG GCC GCC GAA CAA GTA CTC ACC GGA CCT 2909
235 Asp Ser Ser Ile Val Tyr Leu Ala Ala Glu Gln Val Leu Thr Gly Pro
236 30 35 40

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238	GAT	GTA	TCT	GCT	CTG	CAA	TTG	CTC	TCC	AAC	AGC	TTC	GAA	TCC	GTC	TTT	2957
239	Asp	Val	Ser	Ala	Leu	Gln	Leu	Leu	Ser	Asn	Ser	Phe	Glu	Ser	Val	Phe	
240				45					50						55		
242	GAC	TCG	CCG	GAT	GAT	TTC	TAC	AGC	GAC	GCT	AAG	CTT	GTT	CTC	TCC	GAC	3005
243	Asp	Ser	Pro	Asp	Asp	Phe	Tyr	Ser	Asp	Ala	Lys	Leu	Val	Leu	Ser	Asp	
244			60					65					70				
246	GGC	CGG	GAA	GTT	TCT	TTC	CAC	CGG	TGC	GTT	TTG	TCA	GCG	AGA	AGC	TCT	3053
247	Gly	Arg	Glu	Val	Ser	Phe	His	Arg	Cys	Val	Leu	Ser	Ala	Arg	Ser	Ser	
248		75					80					85					
250	TTC	TTC	AAG	AGC	GCT	TTA	GCC	GCC	GCT	AAG	AAG	GAG	AAA	GAC	TCC	AAC	3101
251	Phe	Phe	Lys	Ser	Ala	Leu	Ala	Ala	Ala	Lys	Lys	Glu	Lys	Asp	Ser	Asn	
252	90				95					100						105	
254	AAC	ACC	GCC	GCC	GTG	AAG	CTC	GAG	CTT	AAG	GAG	ATT	GCC	AAG	GAT	TAC	3149
255	Asn	Thr	Ala	Ala	Val	Lys	Leu	Glu	Leu	Lys	Glu	Ile	Ala	Lys	Asp	Tyr	
256				110					115						120		
258	GAA	GTC	GGT	TTC	GAT	TCG	GTT	GTG	ACT	GTT	TTG	GCT	TAT	GTT	TAC	AGC	3197
259	Glu	Val	Gly	Phe	Asp	Ser	Val	Val	Thr	Val	Leu	Ala	Tyr	Val	Tyr	Ser	
260				125					130						135		
262	AGC	AGA	GTG	AGA	CCG	CCG	CCT	AAA	GGA	GTT	TCT	GAA	TGC	GCA	GAC	GAG	3245
263	Ser	Arg	Val	Arg	Pro	Pro	Pro	Lys	Gly	Val	Ser	Glu	Cys	Ala	Asp	Glu	
264			140					145						150			
266	AAT	TGC	TGC	CAC	GTG	GCT	TGC	CGG	CCG	GCG	GTG	GAT	TTC	ATG	TTG	GAG	3293
267	Asn	Cys	Cys	His	Val	Ala	Cys	Arg	Pro	Ala	Val	Asp	Phe	Met	Leu	Glu	
268		155					160						165				
270	GTT	CTC	TAT	TTG	GCT	TTC	ATC	TTC	AAG	ATC	CCT	GAA	TTA	ATT	ACT	CTC	3341
271	Val	Leu	Tyr	Leu	Ala	Phe	Ile	Phe	Lys	Ile	Pro	Glu	Leu	Ile	Thr	Leu	
272	170				175						180					185	
274	TAT	CAG	GTAAACACC	ATCTGCATTA	AGCTATGGTT	ACACATTCAT	GAATATGTTC										3397
275	Tyr	Gln															
278	TTACTTGAGT	ACTTGATTTT	GTATTTTCAG	AGG	CAC	TTA	TTG	GAC	GTT	GTA	GAC						3450
279					Arg	His	Leu	Leu	Asp	Val	Val	Asp					
280								190								195	
282	AAA	GTT	GTT	ATA	GAG	GAC	ACA	TTG	GTT	ATA	CTC	AAG	CTT	GCT	AAT	ATA	3498
283	Lys	Val	Val	Ile	Glu	Asp	Thr	Leu	Val	Ile	Leu	Lys	Leu	Ala	Asn	Ile	
284				200						205					210		
286	TGT	GGT	AAA	GCT	TGT	ATG	AAG	CTA	TTG	GAT	AGA	TGT	AAA	GAG	ATT	ATT	3546
287	Cys	Gly	Lys	Ala	Cys	Met	Lys	Leu	Leu	Asp	Arg	Cys	Lys	Glu	Ile	Ile	
288			215						220					225			
290	GTC	AAG	TCT	AAT	GTA	GAT	ATG	GTT	AGT	CTT	GAA	AAG	TCA	TTG	CCG	GAA	3594
291	Val	Lys	Ser	Asn	Val	Asp	Met	Val	Ser	Leu	Glu	Lys	Ser	Leu	Pro	Glu	
292			230					235						240			
294	GAG	CTT	GTT	AAA	GAG	ATA	ATT	GAT	AGA	CGT	AAA	GAG	CTT	GGT	TTG	GAG	3642
295	Glu	Leu	Val	Lys	Glu	Ile	Ile	Asp	Arg	Arg	Lys	Glu	Leu	Gly	Leu	Glu	
296		245					250					255					
298	GTA	CCT	AAA	GTA	AAG	AAA	CAT	GTC	TCG	AAT	GTA	CAT	AAG	GCA	CTT	GAC	3690
299	Val	Pro	Lys	Val	Lys	Lys	His	Val	Ser	Asn	Val	His	Lys	Ala	Leu	Asp	
300	260				265						270					275	
302	TCG	GAT	GAT	ATT	GAG	TTA	GTC	AAG	TTG	CTT	TTG	AAA	GAG	GAT	CAC	ACC	3738
303	Ser	Asp	Asp	Ile	Glu	Leu	Val	Lys	Leu	Leu	Leu	Lys	Glu	Asp	His	Thr	

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Input Set : N:\Crf3\RULE60\10016236.raw

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304		280		285		290		
306	AAT CTA GAT GAT GCG TGT GCT CTT CAT TTC GCT GTT GCA TAT TGC AAT							3786
307	Asn Leu Asp Asp Ala Cys Ala Leu His Phe Ala Val Ala Tyr Cys Asn							
308		295		300		305		
310	GTG AAG ACC GCA ACA GAT CTT TTA AAA CTT GAT CTT GCC GAT GTC AAC							3834
311	Val Lys Thr Ala Thr Asp Leu Leu Lys Leu Asp Leu Ala Asp Val Asn							
312		310		315		320		
314	CAT AGG AAT CCG AGG GGA TAT ACG GTG CTT CAT GTT GCT GCG ATG CGG							3882
315	His Arg Asn Pro Arg Gly Tyr Thr Val Leu His Val Ala Ala Met Arg							
316		325		330		335		
318	AAG GAG CCA CAA TTG ATA CTA TCT CTA TTG GAA AAA GGT GCA AGT GCA							3930
319	Lys Glu Pro Gln Leu Ile Leu Ser Leu Leu Glu Lys Gly Ala Ser Ala							
320	340		345		350		355	
322	TCA GAA GCA ACT TTG GAA GGT AGA ACC GCA CTC ATG ATC GCA AAA CAA							3978
323	Ser Glu Ala Thr Leu Glu Gly Arg Thr Ala Leu Met Ile Ala Lys Gln							
324		360		365		370		
326	GCC ACT ATG GCG GTT GAA TGT AAT AAT ATC CCG GAG CAA TGC AAG CAT							4026
327	Ala Thr Met Ala Val Glu Cys Asn Asn Ile Pro Glu Gln Cys Lys His							
328		375		380		385		
330	TCT CTC AAA GGC CGA CTA TGT GTA GAA ATA CTA GAG CAA GAA GAC AAA							4074
331	Ser Leu Lys Gly Arg Leu Cys Val Glu Ile Leu Glu Gln Glu Asp Lys							
332		390		395		400		
334	CGA GAA CAA ATT CCT AGA GAT GTT CCT CCC TCT TTT GCA GTG GCG GCC							4122
335	Arg Glu Gln Ile Pro Arg Asp Val Pro Pro Ser Phe Ala Val Ala Ala							
336		405		410		415		
338	GAT GAA TTG AAG ATG ACG CTG CTC GAT CTT GAA AAT AGA G							4162
339	Asp Glu Leu Lys Met Thr Leu Leu Asp Leu Glu Asn Arg							
340	420		425		430			
342	GTATCTATCA AGTCTTATTT CTTATATGTT TGAATTAAAT TTATGTCCTC TCTATTAGGA							4222
344	AACTGAGTGA ACTAATGATA ACTATTCTTT GTGTCGTCCA CTGTTTAG TT GCA CTT							4278
345						Val Ala Leu		
346						435		
348	GCT CAA CGT CTT TTT CCA ACG GAA GCA CAA GCT GCA ATG GAG ATC GCC							4326
349	Ala Gln Arg Leu Phe Pro Thr Glu Ala Gln Ala Ala Met Glu Ile Ala							
350		440		445		450		
352	GAA ATG AAG GGA ACA TGT GAG TTC ATA GTG ACT AGC CTC GAG CCT GAC							4374
353	Glu Met Lys Gly Thr Cys Glu Phe Ile Val Thr Ser Leu Glu Pro Asp							
354		455		460		465		
356	CGT CTC ACT GGT ACG AAG AGA ACA TCA CCG GGT GTA AAG ATA GCA CCT							4422
357	Arg Leu Thr Gly Thr Lys Arg Thr Ser Pro Gly Val Lys Ile Ala Pro							
358		470		475		480		
360	TTC AGA ATC CTA GAA GAG CAT CAA AGT AGA CTA AAA GCG CTT TCT AAA							4470
361	Phe Arg Ile Leu Glu Glu His Gln Ser Arg Leu Lys Ala Leu Ser Lys							
362		485		490		495		
364	ACC G GTATGGATTC TCACCCACTT CATCGGACTC CTTATCACAA AAAACAAAAC							4524
365	Thr							
366	500							
368	TAAATGATCT TTAAACATGG TTTTGTTACT TGCTGTCTGA CCTTGTTTTT TTTATCATCA							4584
370	G TG GAA CTC GGG AAA CGA TTC TTC CCG CGC TGT TCG GCA GTG CTC							4629

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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:18; Xaa Pos.29,34

## VERIFICATION SUMMARY

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Input Set : N:\Crf3\RULE60\10016236.raw

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L:35 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]  
L:36 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]  
L:555 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=3  
L:631 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=4  
L:707 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=5  
L:1417 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9  
L:2159 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=17  
L:2183 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=18  
L:2195 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18 after pos.:16  
L:2198 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18 after pos.:32  
L:2207 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=19  
L:2231 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=20  
L:2252 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=21  
L:2276 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=22  
L:2297 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=23  
L:2321 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=24